

M., Rose, M., Pose, P., Stokes, P., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 RM 309, Biomedical Polymers Research Bldg., 20 S. 2040 E., SIC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0212 row: N column: 07
 Seq primer: CACACAGCAAAACACCTATGACC
 Class: plasmid ends
 High quality sequence stop: 21.

FEATURES

source

1. 21
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="M0067N11"
 /clone_lib="Mouse 10kb plasmid M0067N11 library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, P-"
 /note="Vector: pMD22v. Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adapter oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD22 (g14732114/AF124072.1), a copy number
 inducible derivative of plasmid p1, the vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 0 a 6 c 0 g 15 t
 ORIGIN
 Alignment Scores:
 Pred. No.: 2,940-03 Length: 21
 Score: 25.00 Matches: 5
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0

US-09-856-070-16 (1-5) x A428877 (1-21)

QY 1 GluArgGluIysGlu 5
 Db 15 GAAAGAGAGAGAGAA 1

RESULT 2

AZ336778/c

LOCUS AZ336778 47 bp DNA linear GSS 29-SEP-2000
 DEFINITION M0067N11F Mouse 10kb plasmid M0067N11 F, DNA sequence.
 clone M0067N11 F, DNA sequence.

ACCESSION AZ336778

VERSION AZ336778.1 G1:10406421

KEYWORDS GSS.

SOURCE mouse

ORGANISM Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)
 Contact: Robert B. Weiss
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 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0067 row: N column: 11
 Seq primer: CGTTCGAAAACGACGCCCAT
 Class: plasmid ends
 High quality sequence stop: 37.

FEATURES

source

1. 37
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="M0067N11"
 /clone_lib="Mouse 10kb plasmid M0067N11 library"
 /sex="Male"
 /lab_host="E. coli strain XL10-Gold, TI-resistant, P-"
 /note="Vector: pMD22v. Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adapter oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD22 (g14732114/AF124072.1), a copy number
 inducible derivative of plasmid p1, the vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 8 a 12 c 1 g 16 t
 ORIGIN

Alignment Scores:
 Pred. No.: 4,590-03 Length: 47
 Score: 25.00 Matches: 5
 Percent Similarity: 100.00% Conservativity: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 17 Gaps: 0

US-09-856-070-16 (1-5) x AZ336778 (1-37)

QY 1 GluArgGluIysGlu 5

Db 23 GAAAGAGAGAGAGAA 9

RESULT 3

AZ987023/c

LOCUS

DEFINITION

AZ987023 39 bp DNA linear GSS 27-APR 2001
 M00269N24F Mouse 10kb plasmid M00269N24 F, DNA sequence.
 clone M00269N24 F, DNA sequence.

```

ACCESSION   AZ987023
VERSION     A7987023.1  GI:13958250
KEYWORDS    GSS
SOURCE      house mouse.
ORGANISM    Mus musculus.
REFERENCE   1 (bases 1 to 39)
AUTHORS     Dunham, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Peilly,
            M., Pose, M., Pose, P., Stokes, P., Tingey, A., von Niederhausern, A.,
            and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert R. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunham@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0269 row: N column: 24
            Seq primer: CGTTCTAAACACGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 39
            Location/Qualifiers
                1..39
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="mmcg20020N24"
                /clone_lib="Mouse 10kb plasmid U00C2M library"
                /sex="Female"
                /lab_host="E. coli strain XL10-Gold, 11-resistant, P-"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (g147321141gblAP129072-1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
BASE COUNT   0 a 17 c 1 g 21 t
ORIGIN
Alignment Scores:
Pred. No.: 4,9e+03 Length: 39
Score: 25,00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
US-09-856-070-16 (1-5) x AZ987023 (1-39)
QY 1 GluArgGluTysGlu 5
| | | | | | | | | | |
DB 23 GACAGAGAGAGAG 9

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RESULT 4
ACCESSION   AZ511352
VERSION     LM0356A24F Mouse 10kb plasmid U00C1M library Mus musculus genomic
KEYWORDS    GSS
SOURCE      house mouse.
ORGANISM    Mus musculus.
REFERENCE   1 (bases 1 to 40)
AUTHORS     Dunham, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
            Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Peilly,
            M., Pose, M., Pose, P., Stokes, P., Tingey, A., von Niederhausern, A.,
            and Wright, D., Weiss, R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert R. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunham@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0356 row: A column: 24
            Seq primer: CGTTCTAAACACGCGCCAGT
            Class: plasmid ends
            High quality sequence stop: 40
            Location/Qualifiers
                1..40
                /organism="Mus musculus"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="mmcg1M0356A24"
                /clone_lib="Mouse 10kb plasmid U00C1M library"
                /sex="Male"
                /lab_host="E. coli strain XL10-Gold, 11-resistant, P-"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (g147321141gblAP129072-1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
BASE COUNT   0 a 20 c 0 g 20 t
ORIGIN
Alignment Scores:
Pred. No.: 5e+03 Length: 40
Score: 25,00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
US-09-856-070-16 (1-5) x AZ511352 (1-40)

```

```

QY      1 GluArqGluLysGlu 5
      |||||
DB      21 GACACAGACAGAGAG 7

RESULT 5
A2817465
LOCUS   2000861196 Mouse 10kb plasmid YUGGIM library Mus musculus genomic
DEFINITION
ACCESSION A2817465
VERSION   A2817465.1 GI:12987289
KEYWORDS  house mouse,
SOURCE    Mus musculus
ORGANISM  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
          1 (bases 1 to 42)
REFERENCE 1 (bases 1 to 42)
AUTHORS  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, R., Hamil, C.,
          Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
          M., Rose, M., Reese, F., Stokes, P., Tinney, A., von Nischthausen, A.
          and Wright, D., Weiss, R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
          Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SIC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: rdunn@genetics.utah.edu
          Insert length: 10000 std error: 0 00
          Plate: 0086 row: 1 column: 18
          Seq primer: CACACAGGAAACACATGACC
          Class: plasmid ends
          High quality sequence stop: 42.
FEATURES             source
    location/Qualifiers
        1..42
            /organism="Mus musculus"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGG2M0086118"
            /clone_lib="Mouse 10kb plasmid YUGGIM library"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /note="Vector: pMD20v; Purified genomic DNA from Mus
            musculus (C57BL/6J male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            prepared DNA was purified and stored at 4°C for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pMD2 (ql1472124|3b|AF125072.1), a copy-number
            inducible derivative of plasmid p1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
BASE COUNT          21 a 1 c 15 g 5 t
ORIGIN
Alignment Scores:
Pred. No.:          5,21e-03 Length: 42
Score:              25.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Query Match:        100.00%
DB:                  0

Best Local Similarity: 100.00% Mismatches: 0
Query Match:          100.00% Indels: 0
DB:                    17 Gaps: 0

US-09-856-070-16 (1-5) x A2817465 (1-42)

QY      1 GluArqGluLysGlu 5
      |||||
DB      23 GAGAGGAGAGAGAGAG 37

RESULT 6
AL754610
LOCUS   Arabidopsis thaliana T-DNA flanking sequence GK-054H11-012301,
DEFINITION genomic survey sequence.
ACCESSION AL754610
VERSION   AL754610.1 GI:21487108
KEYWORDS  GSS.
SOURCE    thale cress.
ORGANISM  Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsi.
          1
REFERENCE 1
AUTHORS  Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
          and Weisshaar, B.
          A pipeline for automated high-throughput generation of ESTs
          (flanking sequence tags) from Arabidopsis thaliana T-DNA
          transformed lines
          Unpublished
          2
REFERENCE Rosso, M., Strizhov, N., Li, Y., Peiss, B., Dekker, K. and Weisshaar, B.
          A new Arabidopsis thaliana T-DNA mutagenised population (GAHI-Kat)
          for flanking sequence tag based reverse genetics
          Unpublished
          3 (bases 1 to 48)
REFERENCE Rosso, M., Strizhov, N., Li, Y. and Weisshaar, B.
          Direct Submission
          Submitted (17-JUN-2002) Weisshaar B., Max-Planck Institut fuer
          Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
          This sequence is recovered from the left border of the T-DNA. It
          indicates an insertion close to or within gene Atg51520. The
          sequences are generated at the MPI for Plant Breeding Research in
          the context of the GAHI-Kat project. GAHI-Kat is part of the German
          Plant Genomics program designated 'GAHI'. Information on line
          availability can be found at:
          http://www.mpiz-koeln.mpg.de/GAHI-Kat/.
FEATURES             source
    location/Qualifiers
        1..48
            /organism="Arabidopsis thaliana"
            /strain="Columbia 0"
            /db_xref="taxon:3702"
            /clone="GK-054H11-012301"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            /note="PCR was performed on DNA from Arabidopsis thaliana
            plants (T1) which were transformed with the T-DNA from
            vector pAC161. The lines contain one or more T-DNA
            insertions. The DNA fragment(s) resulting from the PCR
            were directly sequenced to determine the genomic sequence
            flanking the insertion. Sequences displaying significant
            similarity to the A. thaliana nuclear genome sequence were
            processed for submission. T-DNA derived sequences were
            removed"
BASE COUNT          0 a 19 c 3 g 26 t
ORIGIN
Alignment Scores:
Pred. No.:          5,82e-03 Length: 48
Score:              25.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:        100.00% Indels: 0
DB:                  17 Gaps: 0

```


SOURCE: human.
ORGANISM: Homo sapiens
Eukaryota; Metazoa; Chordata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE: 1 (bases 1 to 50)
AUTHORS: Suzuki, Y., Iatani, H., Tsukada, T., Mizushima Sugano, J., Sasaki, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K., Sakaki, Y., Nakamura, Y., Suyama, A., and Sugano, S.
TITLE: Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites
JOURNAL: EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE: 21270072
COMMENT: Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yutaka@iims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A., and Sugano, S. Construction and characterization of a full length enriched and a 5'-end-enriched cDNA library Gene 260 (1-2): 149-156 (1997)

FEATURES
Location/Qualifiers
1..50
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ZRV6C748"
/note="Differential display comparison of untreated and dimethylsulphate treated U937 cells"
BASE COUNT 4 a 19 c 7 q 20 t
ORIGIN

Alignment Scores:
Prod. No.: Length: 6,026+03
Score: 25.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
DB: 9
Gaps: 0

US-09-856-070-16 (1-5) x A0137973 (1-53)
QY 1 GluAragluLysGlu 5
|||||
DB 17 CACAGGCAAAAGAG 3

RESULT 10
AZ638690/c
LOCUS
DEFINITION
AZ638690
GSS.
house mouse.
Mus musculus
ORGANISM

REFERENCE
AUTHORS
Eukaryota; Metazoa, Chordata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Scurionanthi; Muridae; Mus
1 (bases 1 to 51)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmood, M., Meenan, K., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
TITLE: Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL: Unpublished (2000)
COMMENT: Contact: Robert H. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: rdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0498 row: A column: 17
Seq primer: CACACAGGCAAAAGAGGACC
Class: plasmid ends
High quality sequence stop: 51.
Location/Qualifiers
1..51
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0498A17"
/clone_lib="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="R. C. coli strain X10-Gold, T1-resistant, F-"
/note="Vector, pMD42uv, Full-length genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/phenotypes/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.205 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi:4732114|gb|AF129072.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli X10-Gold (Stratagene) cells
and selected for ampicillin resistance."

BASE COUNT 1 a 28 c 0 q 22 t
ORIGIN

Alignment Scores:
Prod. No.: Length: 6,126+03
Score: 25.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
DB: 17
Gaps: 0

US-09-856-070-16 (1-5) x AZ638690 (1-51)
QY 1 GluAragluLysGlu 5
|||||
DB 15 GAAACAGACAAAGAG 1

RESULT 11
AW692145/c
LOCUS
DEFINITION
AW692145
NP052F09ST 5', mRNA sequence.
ACCESSION
AW692145
VERSION
AW692145.2
KEYWORDS
EST.
SOURCE
barrel medic.
MEDICANISM
Medicago truncatula
ORGANISM

REFERENCE
AUTHORS
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, Eudicotyledons; core eudicots;
Posidiales; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 52)
Re, X.-Z., Shadie, G., Scott, A. D., Harris, A. R., Gonzales, R. A., Bell,
C. J., Flores, R. K., Imman, J. T., Weller, J. W., May, G. D., and Dixon,
R. A.
TITLE: Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula stem library
JOURNAL: Unpublished (2000)
COMMENT: On Apr 14, 2003 this sequence version replaced gi:7566881.
Contact: Dixon RA

Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 421 7202
Fax: 580 421 7380
Email: radixon@noble.org

Insert Length: 726 Std Error: 0.00
Plate: 052 row: F column: 09
Seq primer: TCACACAGGAGGAGGTATGAC.

FEATURES

source
1..52
Location/Qualifiers
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF-052P0951"
/clone_lib="developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector, Lambda Zap; Contains a mixture of
intermodal stem segments"

BASE COUNT 8 a 20 c 2 g 22 t
ORIGIN

Alignment Scores:
Pred. No.: 6,22e-03 Length: 52
Score: 25.00 Matches: 5
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-856-070-16 (1-5) x AW692145 (1-52)

QY 1 GluArgGluLysGlu 5
|||||
DB 33 GAAGGAGGAGGAGG 19

RESULT 12
LOCUS BH862110/C 52 bp DNA linear GSS of Arabidopsis
DEFINITION SALK_088796 Arabidopsis thaliana DNA insertion lines Arabidopsis
thaliana genomic clone SALK_088796, DNA sequence.
ACCESSION BH862110
VERSION BH862110.1 GI:22097436
KEYWORDS GSS.
SOURCE thale cress
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 52)

Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab,
J.C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.,
Zimmerman, J. and Ecker, J.R.

A Sequence Indexed Library of Insertion Mutations in the

Arabidopsis Genome

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x752

Fax: 858 558 6379

Email: ecker@salk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At1g04866.

Class: TDNA tagged.

location/Qualifiers

1..52

/organism="Arabidopsis thaliana"

/strain="Columbia"

/db_xref="taxon:3702"

/clone="SALK_088796"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more DNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 11 a 12 c 8 g 21 t
ORIGIN

Alignment Scores:
Pred. No.: 6,22e-03 Length: 52
Score: 25.00 Matches: 5
Percent Similarity: 100.00% Conservatve: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-856-070-16 (1-5) x HH862110 (1-52)

QY 1 GluArgGluLysGlu 5
|||||
DB 29 GAACGGAGAAAGAG 15

RESULT 13

AZ325637/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2000)

Contact: Robert H. Weiss

University of Utah

Genome Center

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0048 row: A column: 11

Seq primer: CCGTGGTAAAGAGGCGGACG

Class: plasmid ends

High quality sequence stop: 53.

location/Qualifiers

1..53

/organism="Mus musculus"

/strain="C57Bl/6J"

/db_xref="taxon:10090"

/clone="JUGGIM0048A11"

/clone_lib="Mouse 10kb plasmid UMGCLM library"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"

/note="Vector: FWD42nv; Purified genomic DNA from M.

musculus C57Bl/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/sequences/shares/>). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and 14

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114 [J6]AP129372.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

```

BASE COUNT      a  24 c  1 g  28 t
ORIGIN
Alignment Scores:
Pred. No.:      6,41e+03      Length:      53
Score:          25.00         Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              17          Gaps:        0

```

US 09 856-070-16 (1-5) x AZ325537 (1-53)

```

QY  1 GluAraqluLysglu 5
DB  22 CACACAGACAGAAAG 8

```

RESULT 14

AZ996539/c

```

LOCUS      AZ996539      54 bp      DNA      linear      GSS      27-APR-2001
DEFINITION 2M02B2F14R Mouse 10kb plasmid 2M02B2F14 R. DNA sequence.

```

ACCESSION AZ996539

VERSION AZ996539.1

KEYWORDS GSS

SOURCE house mouse

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 54)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,

M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausen, A.,

and Wright, D., Weiss, R., Meenen, E., Pedersen, T., Kelly

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah

Medical Polymers Research Bldg., 20 S. 2030 E., StC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: adunn@genetics.utah.edu

Insert length: 10000

Std Error: 0.00

Plate: 6282

Row: F

Column: 14

Seq primer: CACACAGACAGACGATGACC

Class: plasmid ends

High quality sequence step: 54

Location/Qualifiers

1..54

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="2M02B2F14"

/clone_lib="Mouse 10kb plasmid 2M02B2F14"

/sex="Female"

/lab_host="E. coli strain XL10-Gold, II-resistant, F"

/note="Vector: pMD42v; Purified genomic DNA from M.

musculus C57BL/6J (female) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.ncbi.nlm.nih.gov/Genbank/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt ended with 14 DNA polymerase and 14 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114 [J6]AP129372.1); a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance.

```

BASE COUNT      a  21 c  5 g  27 t
ORIGIN
Alignment Scores:
Pred. No.:      6,41e+03      Length:      54
Score:          25.00         Matches:      5
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              17          Gaps:        0

```

US-09-856-070-16 (1-5) x AZ996539 (1-54)

```

QY  1 GluAraqluLysglu 5
DB  34 CACACAGACAGAAAG 20

```

RESULT 15

A1689110

LOCUS A1689110

DEFINITION LX92306.x1 NCI-CGAP-U14 Homo sapiens cDNA clone IMAGE:2277010 4'

similar to TR-064657 Q64657 INTEGRIN BETA 5 SUBUNIT 1, mRNA

sequence.

VERSION A1689110

KEYWORDS EST

SOURCE human

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 55)

AUTHORS NCI-CGAP

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: rstraus@nhi.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert length: 1515

Std Error: 0.00

Seq primer: -400P from Gibco

High quality sequence step: 1.

Location/Qualifiers

1..55

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2277010"

/clone_lib="NCI-CGAP-U14"

/tissue_type="serous papillary carcinoma, high grade, 2

pooled tumors"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site: 1; Salt:
Site_2: Not cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.48 kb. Life Technologies catalog #:
11542-016"

HASE COUNT 31 a 11 c 13 g 0 t

ORIGIN

Alignment Scores:

Pred. No.:	6.51e+03	Length:	55
Score:	25.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-856-070-16 (1-5) x A1689110 (1-55)

QY 1 GluArgGluLysGlu 5

Db 33 GAAAGAGAGAGAGAA 47

Search completed: January 16, 2003, 21:36:58
Job time : 664.571 secs

